SCORE Search Results Details for Application 10552515 and Search Result 20080630_144055_us-10-552-515-4.rag.

This page gives you Search Results detail for the Application 10552515 and Search Result 20080630_144055_us-10-552-515-4.rag.

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GenCore version 6.2.1

OM protein - protein search, using sw model

Run on: June 30, 2008, 17:43:01 ; Search time 71 Seconds
(without alignments)
76.429 Million cell updates/sec

Title: US-10-552-515-4
Perfect score: 42
Sequence: 1 VLLEVVPDV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

9: geneseqp2004b:*
10: geneseqp2005:*
11: geneseqp2006:*
12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	8	ADT77667	Adt77667 Splice va
2	42	100.0	843	10	AEB13424	Aeb13424 Human pro
3	42	100.0	885	10	AEB13426	Aeb13426 Human pro
4	42	100.0	898	4	ABG15488	Abg15488 Novel hum
5	42	100.0	933	8	ADT77664	Adt77664 Splice va
6	42	100.0	933	11	AEL84788	Ael84788 Tumor mar
7	36	85.7	258	2	AAR85775	Aar85775 L. lactis
8	36	85.7	278	5	ABB53746	Abb53746 Lactococc
9	35	83.3	324	6	ABM68555	Abm68555 Photorhab
10	34	81.0	218	10	ABM92385	Abm92385 M. xanthu
11	34	81.0	271	11	AFC47341	Afc47341 Wheat ami
12	34	81.0	292	11	AFC47340	Afc47340 Wheat ami
13	34	81.0	323	11	AFC47339	Afc47339 Wheat ami
14	34	81.0	374	9	AFQ62535	Afq62535 Glycine m
15	34	81.0	407	7	ADM26215	Adm26215 Hyperther
16	34	81.0	440	9	AFQ62538	Afq62538 Glycine m
17	34	81.0	721	4	ABG02181	Abg02181 Novel hum
18	34	81.0	821	7	ADM26833	Adm26833 Hyperther
19	34	81.0	1189	4	ABG03981	Abg03981 Novel hum
20	34	81.0	1189	4	ABG06603	Abg06603 Novel hum
21	34	81.0	1189	4	ABG02166	Abg02166 Novel hum
22	34	81.0	1189	4	ABG07841	Abg07841 Novel hum
23	34	81.0	1189	4	ABG17475	Abg17475 Novel hum
24	34	81.0	1189	4	ABG14742	Abg14742 Novel hum
25	34	81.0	1228	4	ABG23202	Abg23202 Novel hum
26	34	81.0	1259	4	ABG18492	Abg18492 Novel hum
27	34	81.0	1357	4	ABG19664	Abg19664 Novel hum
28	34	81.0	2023	4	ABG06741	Abg06741 Novel hum
29	33	78.6	130	5	AAU81984	Aau81984 Human sec
30	33	78.6	563	8	ADS43542	Ads43542 Bacterial
31	33	78.6	738	10	AEN37939	Aen37939 Dictyoste
32	33	78.6	1112	10	ADV44749	Adv44749 Human nuc
33	33	78.6	1112	12	AEN00030	Aen00030 Human nuc
34	33	78.6	1121	6	ABO07112	Abo07112 Novel hum
35	32	76.2	71	5	ABP01740	Abp01740 Human ORF

36	32	76.2	133	4	AAU58272	Aau58272 Propionib
37	32	76.2	133	6	ABM54791	Abm54791 Propionib
38	32	76.2	145	8	AFQ11484	Afq11484 Glycine m
39	32	76.2	187	9	AFQ55056	Afq55056 Glycine m
40	32	76.2	188	7	ADC95685	Adc95685 E. faeciu
41	32	76.2	206	2	AAW20456	Aaw20456 H. pylori
42	32	76.2	309	4	ABG17090	Abg17090 Novel hum
43	32	76.2	324	5	AAE25510	Aae25510 Kluyverom
44	32	76.2	324	10	AED26279	Aed26279 Novel hum
45	32	76.2	341	7	ADF04428	Adf04428 Bacterial

ALIGNMENTS

RESULT 1
ADT77667
ID ADT77667 standard; peptide; 9 AA.
XX
AC ADT77667;
XX
DT 13-JAN-2005 (first entry)
XX
DE Splice variant-novel gene expressed in prostate (SV-NGEP) epitope.
XX
KW Splice variant-novel gene expressed in prostate; SV-NGEP; human;
KW prostate cancer; cytostatic; gene therapy; immunotherapy; epitope.
XX
OS Homo sapiens.
XX
PN WO2004092213-A1.
XX
PD 28-OCT-2004.
XX
PF 05-APR-2004; 2004WO-US010588.
XX
PR 08-APR-2003; 2003US-0461399P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Pastan I, Bera TK, Lee B;
XX
DR WPI; 2004-758338/74.
XX
PT New Splice Variant-Novel Gene Expressed in Prostate polypeptide or
PT encoding nucleic acid molecule for diagnosing, preventing or treating
PT cancer, especially prostate cancer.
XX
PS Disclosure; SEQ ID NO 4; 88pp; English.

XX
CC The present sequence is that of a predicted epitope of human splice
CC variant-novel gene expressed in prostate (SV-NGEP) ADT77664. The epitope
CC is predicted to bind HLA2-01 and was identified using an HLA binding
CC motif program. It corresponds to amino acids 215-223 of SV-NGEP.
CC Polypeptides comprising an immunogenic fragment of 8 consecutive amino
CC acids of SV-NGEP which specifically bind to an antibody that specifically
CC binds a polypeptide comprising amino acids 157-933 of SV-NGEP are
CC claimed. The invention provides methods for: detecting prostate cancer in
CC a subject by contacting a sample with an antibody that specifically binds
CC a SV-NGEP polypeptide and detecting the formation of an immune complex,
CC or detecting an increase in expression of SV-NGEP polypeptide or mRNA;
CC producing an immune response against a cell expressing SV-NGEP, for
CC example in a subject with prostate cancer, by administering SV-NGEP
CC polypeptide or polynucleotide to produce an immune response that
CC decreases growth of the prostate cancer; inhibiting the growth of a
CC malignant cell that expresses SV-NGEP by culturing cytotoxic T
CC lymphocytes (CTLs) with SV-NGEP to produce activated CTLs, and contacting
CC these with the malignant cell; and inhibiting the growth of a malignant
CC cell by contact with an antibody that specifically binds SV-NGEP, where
CC the antibody is linked to a chemotherapeutic agent or toxin.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 VLLEVVPDV 9
              |||||||||
Db          1 VLLEVVPDV 9
```

RESULT 2
AEB13424
ID AEB13424 standard; protein; 843 AA.
XX
AC AEB13424;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human prostate specific polypeptide #1.
XX
KW Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW cancer; prostate tumor; cytostatic; neoplasm.
XX
OS Homo sapiens.
XX
PN WO2005062788-A2.

XX
PD 14-JUL-2005.
XX
PF 16-DEC-2004; 2004WO-US042406.
XX
PR 22-DEC-2003; 2003US-0531809P.
XX
PA (AVAL-) AVALON PHARM INC.
XX
PI Weigle B, Ebner R;
XX
DR WPI; 2005-497793/50.
DR N-PSDB; AEB13423.
XX
PT Novel isolated prostate specific polypeptide, useful for treating cancer,
PT and identifying agent that modulates activity of cancer related gene.
XX
PS Claim 12; SEQ ID NO 3; 59pp; English.
XX
CC The invention relates to an isolated prostate specific polypeptide
CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous
CC state or potentially cancerous state, an antibody that reacts with a
CC prostate specific polypeptide, an immunoconjugate comprising the antibody
CC and a cytotoxic agent, a method of treating cancer involving contacting a
CC cancerous cell in vivo with an agent having activity against a prostate
CC specific polypeptide and an immunogenic composition the prostate specific
CC polypeptide. The prostate specific polypeptide is useful for identifying
CC an agent that modulates the activity of a cancer related gene. The
CC immunogenic composition is useful for treating cancer, preferably
CC prostate cancer in an animal, e.g. human, which involves administering
CC the immunogenic composition that is sufficient to elicit the production
CC of cytotoxic T lymphocytes specific for the prostate specific
CC polypeptide. The invention is useful for identifying anti-neoplastic
CC agents. This sequence represents a human prostate specific polypeptide of

```
CC   the invention.
XX
SQ   Sequence 843 AA;

  Query Match             100.0%;  Score 42;  DB 10;  Length 843;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLLEVVPDV 9
              |||||||||
Db        216 VLLEVVPDV 224


RESULT 3
AEB13426
ID   AEB13426 standard; protein; 885 AA.
XX
AC   AEB13426;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human prostate specific polypeptide #2.
XX
KW   Screening; diagnosis; drug delivery; prostate specific polypeptide;
KW   cancer; prostate tumor; cytostatic; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO2005062788-A2.
XX
PD   14-JUL-2005.
XX
PF   16-DEC-2004; 2004WO-US042406.
XX
PR   22-DEC-2003; 2003US-0531809P.
XX
PA   (AVAL-) AVALON PHARM INC.
XX
PI   Weigle B,  Ebner R;
XX
DR   WPI; 2005-497793/50.
DR   N-PSDB; AEB13425.
XX
PT   Novel isolated prostate specific polypeptide, useful for treating cancer,
PT   and identifying agent that modulates activity of cancer related gene.
XX
PS   Claim 12; SEQ ID NO 5; 59pp; English.
XX
CC   The invention relates to an isolated prostate specific polypeptide
```

CC comprising one or more immunogenic fragments. The invention also relates
CC to a method of identifying an agent that modulates the activity of a
CC cancer related gene involving contacting a compound with a cell
CC containing a gene under conditions promoting the expression of the gene,
CC detecting a difference in expression of the gene relative to when the
CC compound is not present and identifying an agent that modulates the
CC activity of a cancer related gene, a method of identifying an anti-
CC neoplastic agent involving contacting a cell exhibiting neoplastic
CC activity with a compound first identified as a cancer related gene
CC modulator using and determining a decrease in neoplastic activity after
CC contacting, when compared to when the contacting does not occur, or
CC administering an agent first identified to an animal exhibiting a cancer
CC condition and detecting a decrease in cancerous condition, a method of
CC determining the cancerous status of a cell involving determining an
CC increase in the level of expression in a cell of a gene where an elevated
CC expression relative to a known non-cancerous cell indicates a cancerous
CC state or potentially cancerous state, an antibody that reacts with a
CC prostate specific polypeptide, an immunoconjugate comprising the antibody
CC and a cytotoxic agent, a method of treating cancer involving contacting a
CC cancerous cell in vivo with an agent having activity against a prostate
CC specific polypeptide and an immunogenic composition the prostate specific
CC polypeptide. The prostate specific polypeptide is useful for identifying
CC an agent that modulates the activity of a cancer related gene. The
CC immunogenic composition is useful for treating cancer, preferably
CC prostate cancer in an animal, e.g. human, which involves administering
CC the immunogenic composition that is sufficient to elicit the production
CC of cytotoxic T lymphocytes specific for the prostate specific
CC polypeptide. The invention is useful for identifying anti-neoplastic
CC agents. This sequence represents a human prostate specific polypeptide of
CC the invention.
XX
SQ Sequence 885 AA;

Query Match 100.0%; Score 42; DB 10; Length 885;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 VLLEVVPDV 9
              |||||||||
Db        216 VLLEVVPDV 224
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RESULT 4
ABG15488
ID ABG15488 standard; protein; 898 AA.
XX
AC ABG15488;
XX
DT 18-FEB-2002 (first entry)

XX
DE Novel human diagnostic protein #15479.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS79675.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 45847; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this

```
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 898 AA;

  Query Match             100.0%;  Score 42;  DB 4;  Length 898;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLLEVVPDV 9
              |||||||||
Db        308 VLLEVVPDV 316


RESULT 5
ADT77664
ID   ADT77664 standard; protein; 933 AA.
XX
AC   ADT77664;
XX
DT   15-JUN-2007  (revised)
DT   13-JAN-2005  (first entry)
XX
DE   Splice variant-novel gene expressed in prostate (SV-NGEP) polypeptide.
XX
KW   Splice variant-novel gene expressed in prostate; SV-NGEP; human;
KW   prostate cancer; cytostatic; gene therapy; immunotherapy; BOND_PC;
KW   NGEP long variant; NGEP long variant [Homo sapiens]; GO5886.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .345
FT                   /label= Cytoplasmic
FT   Region          157. .933
FT                   /note= "An immunogenic fragment comprising 8 consecutive
FT                   amino acids that specifically binds to an antibody that
FT                   specifixally binds to a polypeptide comprising amino
FT                   acids 157-933 is referred to in Claim 1"
FT   Region          170. .178
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          215. .223
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          258. .266
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          346. .368
FT                   /label= Transmembrane
FT   Domain          369. .421
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FT                   /label= External
FT                   /note= "Cell surface"
FT   Region          403. .411
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          422. .441
FT                   /label= Transmembrane
FT   Region          427. .435
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          442. .501
FT                   /label= Cytoplasmic
FT   Domain          502. .524
FT                   /label= Transmembrane
FT   Domain          525. .543
FT                   /label= External
FT                   /note= "Cell surface"
FT   Domain          544. .566
FT                   /label= Transmembrane
FT   Region          557. .565
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Region          562. .570
FT                   /note= "Epitope, predicted to bind HLA2-01"
FT   Domain          567. .586
FT                   /label= Cytoplasmic
FT   Domain          587. .609
FT                   /label= Transmembrane
FT   Domain          610. .714
FT                   /label= External
FT                   /note= "Cell surface"
FT   Domain          715. .737
FT                   /label= Transmembrane
FT   Domain          738. .761
FT                   /label= Cytoplasmic
FT   Domain          762. .784
FT                   /label= Transmembrane
FT   Domain          785. .933
FT                   /label= External
FT                   /note= "Cell surface"
FT   Region          846. .854
FT                   /note= "Epitope, predicted to bind HLA2-01"
XX
PN   WO2004092213-A1.
XX
PD   28-OCT-2004.
XX
PF   05-APR-2004; 2004WO-US010588.
XX
PR   08-APR-2003; 2003US-0461399P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
```

XX
PI Pastan I, Bera TK, Lee B;
XX
DR WPI; 2004-758338/74.
DR N-PSDB; ADT77665.
DR PC:NCBI; gi48093524.
XX
PT New Splice Variant-Novel Gene Expressed in Prostate polypeptide or
PT encoding nucleic acid molecule for diagnosing, preventing or treating
PT cancer, especially prostate cancer.
XX
PS Claim 1; SEQ ID NO 1; 88pp; English.
XX
CC The present sequence is the protein sequence of splice variant-novel gene
CC expressed in prostate (SV-NGEP). SV-NGEP is identical to NGEP from amino
CC acid 1-157, diverging from amino acid 158. Expression analysis in 76
CC normal and foetal tissues showed SV-NGEP to be strongly expressed only in
CC a prostate sample. Claimed methods for detecting prostate cancer in a
CC subject comprise: contacting the sample with an antibody that
CC specifically binds a SV-NGEP polypeptide and detecting the formation of
CC an immune complex; or detecting an increase in expression of SV-NGEP
CC polypeptide or mRNA. Antibodies to an SV-NGEP polypeptide can be used to
CC detect metastatic prostate cancer cells at locations other than the
CC prostate. A claimed method for producing an immune response against a
CC cell expressing SV-NGEP, for example in a subject with prostate cancer,
CC comprises administering the polypeptide, or a polynucleotide encoding it,
CC to produce an immune response that decreases growth of the prostate
CC cancer. A claimed method for inhibiting the growth of a malignant cell
CC that expresses SV-NGEP comprises culturing cytotoxic T lymphocytes (CTLs)
CC with SV-NGEP to produce activated CTLs that recognise an NGEP expressing
CC cell, and contacting the malignant cell with the activated CTLs.
CC Alternatively, growth of a malignant cell is inhibited by contact with an
CC antibody that specifically binds an SV-NGEP polypeptide, where the
CC antibody is linked to an effector molecule (chemotherapeutic agent or
CC toxin) that inhibits growth of the malignant cell. This may be performed
CC in vivo. Kits for detecting an SV-NGEP polypeptide or polynucleotide in a
CC sample are also claimed.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 42; DB 8; Length 933;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VLLEVVPDV 9
              |||||||||
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```
Db        215 VLLEVVPDV 223


RESULT 6
AEL84788
ID   AEL84788 standard; protein; 933 AA.
XX
AC   AEL84788;
XX
DT   18-OCT-2007  (revised)
DT   15-JUN-2007  (revised)
DT   28-DEC-2006  (first entry)
XX
DE   Tumor marker gene NGEP SEQ ID NO 155.
XX
KW   cytostatic; diagnosis; prognosis; tumor marker; gene expression;
KW   drug screening; cancer; neoplasm; NGEP; BOND_PC; NGEP long variant;
KW   GO5886.
XX
OS   Homo sapiens.
XX
PN   WO2006110593-A2.
XX
PD   19-OCT-2006.
XX
PF   07-APR-2006; 2006WO-US013172.
XX
PR   07-APR-2005; 2005US-0669342P.
PR   11-OCT-2005; 2005US-0725982P.
XX
PA   (MACR-) MACROGENICS INC.
XX
PI   Von Haller PD,  Schummer M,  Meyer DW,  Schubert LA,  Tjoelker LW;
XX
DR   WPI; 2006-814687/82.
DR   N-PSDB; AEL84787.
DR   REFSEQ; NP_001001891.
DR   PC:NCBI; gi48093524.
XX
PT   Detecting or diagnosing cancer in a subject comprises determining
PT   expression of at least one gene, and comparing level of expression to a
PT   control sample from a normal subject, where increased expression level
PT   indicates cancer.
XX
PS   Claim 8; SEQ ID NO 155; 583pp; English.
XX
CC   The invention describes a method of detecting or diagnosing cancer in a
CC   subject comprising determining the expression level of at least one gene,
CC   and comparing the level of expression to a corresponding control sample
```

CC from a normal subject, where cancer is detected or diagnosed if there is
CC an increase in the expression level of the gene relative to the
CC expression in the control sample. Also described are: identifying a
CC compound to be tested for its ability to prevent, treat, manage, or
CC ameliorate cancer or its symptom; a compound identified by the method;
CC treating cancer in a patient; treating a cancer in a subject that is
CC fully or partially refractory to a first treatment in a patient; and a
CC pharmaceutical composition comprising an amount of an antibody selected
CC from anti-SLC12A2, anti-FLJ23375, anti-GRM5, anti-TAS2R1, anti-NRXN2,
CC anti-C14orf160, anti-MGC 15668, anti-MGC33486, anti-TMEM16F, anti-FAT,
CC anti-KIAA0195, anti-LRFN, anti-NFASC, anti-BAT2Dl, anti-MGC2963, anti-
CC KIAA0685, anti-EDG3, anti-GGTL3, anti-PLVAP, anti-FLJ31528, anti-
CC FLJ90709, anti-VEZATIN, anti-TMPRSS9, anti-ATP13A5, anti-PKHD1L1, anti-
CC C2orf18, anti-ANKRD22, anti-FAM62B, anti-LOC57168, anti-CDKAL1, anti-
CC SLC39A3v1, anti-SLC39A3v2, anti-BAT5, anti-TM9SF4, anti-DC2, anti-VAPB,
CC anti-XTP3TPB, anti-TACSTD2, anti-FNDC3A, anti-GK001, anti-OCIAD2, anti-
CC PR01855, anti-C20orf3, anti-SDFR1, anti-FLJ20481, anti-LENG4, anti-
CC FLJ12443, anti-ARP5 Long, anti-ARP5 Short, anti-TMD0645, anti-NGEP, anti-
CC IL1RAP1, anti-PLXNB1, anti-ATP2B2, anti~FLJ11848, anti-ENTPD2, anti-
CC PPM1H, anti-KRTKAP3, anti-KCNC3, anti-TM9SF1, anti-ULBP1, anti-C19orf26,
CC anti-KIAA830, anti-KIAA1244, anti-KIAA1797, anti-MGC26856, anti-NETO2,
CC anti-SUSD2, anti-FOLR2, anti-EMR2, ENTPD1, anti-ATP10B, anti-PTK7, anti-
CC FLJ14681, anti-C20orf22, anti-FLJ14281, anti-FAM8A1, anti-TMED7, anti-
CC C20orf108, anti-ATAD1, anti-GPR154, anti-C14orf27, anti-OSAP, anti-
CC FAD104, anti-FLJ90492, anti-SLC27A3, anti-RON, anti-ATP13A1, anti-
CC DKFZP564D166, anti-ESSPL, anti-EXTL3, anti-KAI1, anti-KIAA0960, anti-
CC MTRNL, anti-SLC27A1, anti-GRIA, anti-OR4M1, anti-KIAA1679, or anti-UPK-1b
CC antibody, and a pharmaceutical carrier. The methods are useful for
CC detecting, diagnosing, and treating cancer, e.g. colon, lung, ovary,
CC prostate, pancreas, or bladder cancer. This is the amino acid sequence of
CC NGEP, altered levels of expression are useful in the diagnosis or
CC prognosis of cancer.
CC
CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 933 AA;

Query Match 100.0%; Score 42; DB 11; Length 933;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 VLLEVVPDV 9
              |||||||||
Db        215 VLLEVVPDV 223
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RESULT 7
AAR85775

ID   AAR85775 standard; protein; 258 AA.
XX
AC   AAR85775;
XX
DT   16-OCT-2003 (revised)
DT   27-AUG-2003 (revised)
DT   25-AUG-1996 (first entry)
XX
DE   L. lactis phage R1-t repressor protein.
XX
KW   Lactococcus lactis; lactic acid bacterium; promoter; repressor; flavour;
KW   food.
XX
OS   Bacteriophage r1t; Type P335.
XX
PN   WO9531563-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-NL000172.
XX
PR   12-MAY-1994;   94EP-00201355.
XX
PA   (UNIL) QUEST INT BV.
XX
PI   Nauta A, Venema G, Kok J, Ledeboer AM;
XX
DR   WPI; 1996-010948/01.
DR   N-PSDB; AAT02612.
XX
PT   Complex inducible promoter system from lactic acid bacterium phage - also
PT   modified forms with inactivated repressor gene, allowing production of
PT   proteins in food grade microorganisms.
XX
PS   Disclosure; Page 33-35; 53pp; English.
XX
CC   A complex inducible promoter system (AAT02612) is derived from phage R1-t
CC   of Lactococcus lactis subsp. cremoris. The system includes ORF27, the rro
CC   gene, that codes for a protein (AAR85775) capable of repressing gene
CC   expression. This regulatory region can be exploited for the construction
CC   of thermo-inducible gene expression systems in L. lactis, allowing prodn.
CC   of recombinant proteins by this food-grade microorganism. ORF27 is in
CC   opposite orientation to ORF28 (tec) and ORF29. If an inactivating
CC   mutation is introduced into the rro product, then ORF29 is expressed
CC   constitutively at high level. (Updated on 27-AUG-2003 to correct OS
CC   field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 258 AA;

```
  Query Match             85.7%;  Score 36;  DB 2;  Length 258;
  Best Local Similarity   77.8%;  Pred. No. 97;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLLEVVPDV 9
              ||:| ||||
Db        189 VLIEAVPDV 197



RESULT 8
ABB53746
ID   ABB53746 standard; protein; 278 AA.
XX
AC   ABB53746;
XX
DT   15-JUN-2007  (revised)
DT   29-AUG-2003  (revised)
DT   16-MAY-2002  (first entry)
XX
DE   Lactococcus lactis protein pil03.
XX
KW   Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; BOND_PC;
KW   repressor; repressor [Bacteriophage bIL309]; cI-like;
KW   repressor [Lactococcus phage bIL309]; prophage pi1 protein 03;
KW   prophage pi1 protein 03 [Lactococcus lactis subsp. lactis Il1403]; pi103;
KW   prophage pi1 protein 03, transcriptional regulator;
KW   repressor [bacteriophage bIL309].
XX
OS   Lactococcus lactis; IL1403.
XX
PN   FR2807446-A1.
XX
PD   12-OCT-2001.
XX
PF   11-APR-2000; 2000FR-00004630.
XX
PR   11-APR-2000; 2000FR-00004630.
XX
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
PI   Bolotine A,  Sorokine A,  Renault P,  Ehrlich SD;
XX
DR   WPI; 2002-043418/06.
DR   PC:NCBI; gi12723316.
XX
PT   New nucleotide sequence useful in the identification or Lactococcus
PT   lactis and related species.
XX
PS   Claim 6; SEQ ID NO 448; 2504pp; French.
```

```
XX
CC   The present invention is related to a Lactococcus lactis nucleotide
CC   sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic
CC   acid sequence is useful in the detection and/or amplification of nucleic
CC   acid sequence, particularly to identify Lactococcus lactis or related
CC   species. The proteins of the invention are useful for the biosynthesis or
CC   biodegradation of a composition of interest. The invention helps research
CC   in lactic bacteria, particularly useful in the production of yogurt and
CC   cheese. Note: The sequence data for this patent is based on equivalent
CC   patent WO200177334 (published 18-OCT-2001) which is available in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
CC   standardise OS field)
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 278 AA;

  Query Match             85.7%;  Score 36;  DB 5;  Length 278;
  Best Local Similarity   77.8%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLLEVVPDV 9
              ||:| ||||
Db        209 VLIEAVPDV 217


RESULT 9
ABM68555
ID   ABM68555 standard; protein; 324 AA.
XX
AC   ABM68555;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Photorhabdus luminescens protein sequence #1652.
XX
KW   Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW   detection; food; gene expression; plant; animal; microorganism; toxin;
KW   antibiotic; biopesticide; virulence factor; disease model; plague;
KW   whooping cough.
XX
OS   Photorhabdus luminescens.
XX
PN   WO200294867-A2.
XX
PD   28-NOV-2002.
XX
```

PF 07-FEB-2002; 2002WO-IB003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
DR WPI; 2003-148459/14.
XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 1652; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins
XX
SQ Sequence 324 AA;

  Query Match   83.3%; Score 35; DB 6; Length 324;
  Best Local Similarity   77.8%; Pred. No. 2e+02;
  Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

```
Qy          1 VLLEVVPDV 9
              |||| |||:
Db        149 VLLEAVPDL 157
```

```
RESULT 10
ABM92385
ID   ABM92385 standard; protein; 218 AA.
XX
AC   ABM92385;
XX
DT   02-JUN-2005  (first entry)
XX
DE   M. xanthus protein sequence, seq id 11584.
XX
KW   Transgenic plant; DNA replication; gene regulation; gene expression.
XX
OS   Myxococcus xanthus.
XX
PN   US6833447-B1.
XX
PD   21-DEC-2004.
XX
PF   10-JUL-2001; 2001US-00902540.
XX
PR   10-JUL-2000; 2000US-0217883P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Goldman BS,  Hinkle GJ,  Slater SC,  Wiegand RC;
XX
DR   WPI; 2005-028716/03.
XX
PT   New substantially purified Myxococcus xanthus nucleic acid molecule
PT   encoding a nitrite reductase, useful for determining gene expression,
PT   identifying mutations in a gene of interest, and for constructing
PT   mutations in a gene of interest.
XX
PS   Example 2; SEQ ID NO 11584; 25pp; English.
XX
CC   The invention relates to a substantially purified nucleic acid molecule
CC   encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC   recombinant DNA construct for expression of a nitrite reductase gene in a
CC   plant cell, and a plant cell comprising the recombinant DNA construct.
CC   The nucleic acid is useful for determining gene expression, identifying
CC   mutations in a gene of interest, and for constructing mutations in a gene
CC   of interest. Sequences given in records for SEQ IDs 9692-16825 represent
CC   a group of 7134 Mxyococcus xanthus proteins and peptides. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO
XX
SQ   Sequence 218 AA;
```

```
  Query Match             81.0%;  Score 34;  DB 10;  Length 218;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLLEVVPDV 9
              || ||:|||
Db        117 VLAEVLPDV 125
```

```
RESULT 11
AFC47341
ID   AFC47341 standard; protein; 271 AA.
XX
AC   AFC47341;
XX
DT   20-SEP-2007  (first entry)
XX
DE   Wheat amino acid sequence SEQ ID NO 8711.
XX
KW   plant; DNA mapping; gene expression.
XX
OS   Triticum aestivum.
XX
PN   US2006048240-A1.
XX
PD   02-MAR-2006.
XX
PF   01-APR-2005; 2005US-00096568.
XX
PR   01-APR-2004; 2004US-0558095P.
XX
PA   (ALEX/) ALEXANDROV N.
PA   (BROV/) BROVER V.
XX
PI   Alexandrov N,  Brover V;
XX
DR   WPI; 2006-421739/43.
XX
PT   New isolated Sequence-Determined DNA Fragments (SDFs) from different
PT   plant species, e.g. corn, wheat, soybean, or rice, useful for controlling
PT   behavior of a gene in the chromosome or identifying a particular
PT   individual organism.
XX
PS   Claim 9; SEQ ID NO 8711; 87pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule from the
CC   genome of a plant. Also described: (1) a vector construct comprising: (a)
CC   a first nucleic acid having a regulatory sequence capable of causing
CC   transcription and/or translation; and (b) a second nucleic acid having
```

```
CC   the sequence of the isolated nucleic acid molecule above, where the first
CC   and second nucleic acids are operably linked, and where the second
CC   nucleic acid is heterologous to any element in the vector construct; (2)
CC   a host cell comprising the isolated nucleic acid molecule above, where
CC   the nucleic acid molecule is flanked by an exogenous sequence, or
CC   comprising the vector construct above; (3) an isolated polypeptide
CC   comprising an amino acid sequence: (a) exhibiting at least 40-90%
CC   sequence identity of an amino acid sequence encoded by a sequence given
CC   in the specification or the Sequence Listing, or its fragment; and (b)
CC   capable of exhibiting at least one of the biological activities of the
CC   polypeptide encoded by the nucleotide sequence in (a); (4) an antibody
CC   capable of binding the isolated polypeptide; (5) introducing an isolated
CC   nucleic acid into a host cell; (6) transforming a host cell; (7)
CC   modulating transcription and/or translation of the nucleic acid in a host
CC   cell; (8) detecting a nucleic acid in a sample; (9) a plant or cell of a
CC   plant comprising the nucleic acid molecule, which is exogenous or
CC   heterologous to the plant or plant cell, or comprising the vector
CC   construct above; and (10) a plant regenerated from the plant cell above.
CC   The nucleic acids are useful for specifying a gene product in cells,
CC   either as a promoter or as a protein coding sequence or as an UTR or as a
CC   3' termination sequence. They are also useful in controlling the behavior
CC   of a gene in the chromosome, controlling the expression of a gene or as
CC   tools for genetic mapping, recognizing or isolating identical or related
CC   DNA fragments, or identifying a particular individual organism, or
CC   clustering of a group of organisms with a common trait. The present
CC   sequence represents a specifically claimed wheat amino acid sequence from
CC   the present invention. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from the USPTO web site.
XX
SQ   Sequence 271 AA;

  Query Match             81.0%;  Score 34;  DB 11;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LEVVPDV 9
              |||||||
Db         27 LEVVPDV 33


RESULT 12
AFC47340
ID   AFC47340 standard; protein; 292 AA.
XX
AC   AFC47340;
XX
DT   20-SEP-2007  (first entry)
XX
```

DE Wheat amino acid sequence SEQ ID NO 8710.
XX
KW plant; DNA mapping; gene expression.
XX
OS Triticum aestivum.
XX
PN US2006048240-A1.
XX
PD 02-MAR-2006.
XX
PF 01-APR-2005; 2005US-00096568.
XX
PR 01-APR-2004; 2004US-0558095P.
XX
PA (ALEX/) ALEXANDROV N.
PA (BROV/) BROVER V.
XX
PI Alexandrov N, Brover V;
XX
DR WPI; 2006-421739/43.
XX
PT New isolated Sequence-Determined DNA Fragments (SDFs) from different
PT plant species, e.g. corn, wheat, soybean, or rice, useful for controlling
PT behavior of a gene in the chromosome or identifying a particular
PT individual organism.
XX
PS Claim 9; SEQ ID NO 8710; 87pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule from the
CC genome of a plant. Also described: (1) a vector construct comprising: (a)
CC a first nucleic acid having a regulatory sequence capable of causing
CC transcription and/or translation; and (b) a second nucleic acid having
CC the sequence of the isolated nucleic acid molecule above, where the first
CC and second nucleic acids are operably linked, and where the second
CC nucleic acid is heterologous to any element in the vector construct; (2)
CC a host cell comprising the isolated nucleic acid molecule above, where
CC the nucleic acid molecule is flanked by an exogenous sequence, or
CC comprising the vector construct above; (3) an isolated polypeptide
CC comprising an amino acid sequence: (a) exhibiting at least 40-90%
CC sequence identity of an amino acid sequence encoded by a sequence given
CC in the specification or the Sequence Listing, or its fragment; and (b)
CC capable of exhibiting at least one of the biological activities of the
CC polypeptide encoded by the nucleotide sequence in (a); (4) an antibody
CC capable of binding the isolated polypeptide; (5) introducing an isolated
CC nucleic acid into a host cell; (6) transforming a host cell; (7)
CC modulating transcription and/or translation of the nucleic acid in a host
CC cell; (8) detecting a nucleic acid in a sample; (9) a plant or cell of a
CC plant comprising the nucleic acid molecule, which is exogenous or
CC heterologous to the plant or plant cell, or comprising the vector

CC construct above; and (10) a plant regenerated from the plant cell above.
CC The nucleic acids are useful for specifying a gene product in cells,
CC either as a promoter or as a protein coding sequence or as an UTR or as a
CC 3' termination sequence. They are also useful in controlling the behavior
CC of a gene in the chromosome, controlling the expression of a gene or as
CC tools for genetic mapping, recognizing or isolating identical or related
CC DNA fragments, or identifying a particular individual organism, or
CC clustering of a group of organisms with a common trait. The present
CC sequence represents a specifically claimed wheat amino acid sequence from
CC the present invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the USPTO web site.
XX
SQ Sequence 292 AA;

Query Match 81.0%; Score 34; DB 11; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 LEVVPDV 9
              |||||||
Db         48 LEVVPDV 54
```

RESULT 13
AFC47339
ID AFC47339 standard; protein; 323 AA.
XX
AC AFC47339;
XX
DT 20-SEP-2007 (first entry)
XX
DE Wheat amino acid sequence SEQ ID NO 8709.
XX
KW plant; DNA mapping; gene expression.
XX
OS Triticum aestivum.
XX
PN US2006048240-A1.
XX
PD 02-MAR-2006.
XX
PF 01-APR-2005; 2005US-00096568.
XX
PR 01-APR-2004; 2004US-0558095P.
XX
PA (ALEX/) ALEXANDROV N.
PA (BROV/) BROVER V.
XX

PI Alexandrov N, Brover V;
XX
DR WPI; 2006-421739/43.
XX
PT New isolated Sequence-Determined DNA Fragments (SDFs) from different
PT plant species, e.g. corn, wheat, soybean, or rice, useful for controlling
PT behavior of a gene in the chromosome or identifying a particular
PT individual organism.
XX
PS Claim 9; SEQ ID NO 8709; 87pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule from the
CC genome of a plant. Also described: (1) a vector construct comprising: (a)
CC a first nucleic acid having a regulatory sequence capable of causing
CC transcription and/or translation; and (b) a second nucleic acid having
CC the sequence of the isolated nucleic acid molecule above, where the first
CC and second nucleic acids are operably linked, and where the second
CC nucleic acid is heterologous to any element in the vector construct; (2)
CC a host cell comprising the isolated nucleic acid molecule above, where
CC the nucleic acid molecule is flanked by an exogenous sequence, or
CC comprising the vector construct above; (3) an isolated polypeptide
CC comprising an amino acid sequence: (a) exhibiting at least 40-90%
CC sequence identity of an amino acid sequence encoded by a sequence given
CC in the specification or the Sequence Listing, or its fragment; and (b)
CC capable of exhibiting at least one of the biological activities of the
CC polypeptide encoded by the nucleotide sequence in (a); (4) an antibody
CC capable of binding the isolated polypeptide; (5) introducing an isolated
CC nucleic acid into a host cell; (6) transforming a host cell; (7)
CC modulating transcription and/or translation of the nucleic acid in a host
CC cell; (8) detecting a nucleic acid in a sample; (9) a plant or cell of a
CC plant comprising the nucleic acid molecule, which is exogenous or
CC heterologous to the plant or plant cell, or comprising the vector
CC construct above; and (10) a plant regenerated from the plant cell above.
CC The nucleic acids are useful for specifying a gene product in cells,
CC either as a promoter or as a protein coding sequence or as an UTR or as a
CC 3' termination sequence. They are also useful in controlling the behavior
CC of a gene in the chromosome, controlling the expression of a gene or as
CC tools for genetic mapping, recognizing or isolating identical or related
CC DNA fragments, or identifying a particular individual organism, or
CC clustering of a group of organisms with a common trait. The present
CC sequence represents a specifically claimed wheat amino acid sequence from
CC the present invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the USPTO web site.
XX
SQ Sequence 323 AA;

Query Match 81.0%; Score 34; DB 11; Length 323;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;

```
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LEVVPDV 9
              |||||||
Db         79 LEVVPDV 85
```

RESULT 14
AFQ62535
ID   AFQ62535 standard; protein; 374 AA.
XX
AC   AFQ62535;
XX
DT   18-OCT-2007 (first entry)
XX
DE   Glycine max protein SEQ ID NO:253712.
XX
KW   plant; cold tolerance; heat tolerance; drought resistance;
KW   herbicide resistance; pathogen resistance; pesticide resistance;
KW   disease-resistance; crop improvement; insect resistance;
KW   nitrogen fixation; plant growth regulation; plant disease;
KW   stress tolerance; seed oil; transgenic.
XX
OS   Glycine max.
XX
PN   US2004031072-A1.
XX
PD   12-FEB-2004.
XX
PF   28-APR-2003; 2003US-00424599.
XX
PR   06-MAY-1999;   99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LROS/) LA ROSA T J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (CAOY/) CAO Y.
XX
PI   La Rosa TJ, Zhou Y, Kovalic DK, Cao Y;
XX
DR   WPI; 2004-168999/16.
XX
PT   New recombinant DNA construct, useful in producing plants with desired
PT   properties, e.g. increased cold, heat or drought tolerance or tolerance
PT   to herbicides, extreme osmotic conditions or pathogens and improved plant
PT   growth and development.
XX
PS   Claim 2; SEQ ID NO 253712; 15pp; English.

XX
CC The invention relates to a recombinant DNA construct, polynucleotides or
CC polypeptides which are useful in improving plant cold, heat or drought
CC tolerance or tolerance to herbicides, extreme osmotic conditions,
CC pathogens or pests, in improving yield by modification of photosynthesis
CC or of carbohydrate, nitrogen or phosphorus use and/or uptake, in
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, in providing increased resistance to plant disease and improved
CC plant growth and development under at least one stress condition, in
CC producing galactomannan, plant growth regulators and lignin, in
CC increasing the rate of homologous recombination in plants, in modifying
CC seed oil yield and/or content and seed protein yield and/or content and
CC in encoding a plant transcription factor. The present sequence represents
CC a Glycine max protein of the invention. Note: This sequence is not shown
CC in the specification but was obtained in electronic format directly from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 374 AA;

Query Match 81.0%; Score 34; DB 9; Length 374;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLEVVPD 8
|:|||:||
Db 243 VVLEVIPD 250

RESULT 15
ADM26215
ID ADM26215 standard; protein; 407 AA.
XX
AC ADM26215;
XX
DT 20-MAY-2004 (first entry)
XX
DE Hyperthermophile Methanopyrus kandleri protein #821.
XX
KW hyperthermophile; protein stability enhancement;
KW protein activity enhancement.
XX
OS Methanopyrus kandleri.
XX
PN WO2003076575-A2.
XX
PD 18-SEP-2003.
XX
PF 04-MAR-2003; 2003WO-US006664.
XX

PR 04-MAR-2002; 2002US-0361742P.
PR 14-MAY-2002; 2002US-0380423P.
PR 16-SEP-2002; 2002US-0410974P.
XX
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
XX
PI Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;
XX
DR WPI; 2003-748383/70.
DR N-PSDB; ADM27081.
XX
PT New isolated nucleic acids encoding any of about 1700 Methanopyrus
PT kandleri proteins, and the encoded proteins, useful as a medicaments or
PT as diagnostic agents.
XX
PS Claim 31; SEQ ID NO 821; 1023pp; English.
XX
CC The invention comprises the amino acid sequence of proteins from the
CC hyperthermophile Methanopyrus kandleri, the invention also comprises the
CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri
CC proteins of the invention are useful for enhancing the stability and/or
CC activity of other proteins. The Methanopyrus kandleri genome is useful in
CC a variety of diagnostic and analytical methods. The present amino acid
CC sequence represents a Methanopyrus kandleri protein of the invention.
XX
SQ Sequence 407 AA;

Query Match 81.0%; Score 34; DB 7; Length 407;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 LLEVVPDV 9
              |||:|||:
Db        199 LLEIVPDL 206
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Search completed: June 30, 2008, 17:53:04
Job time : 75.875 secs